homologous genes from DNA or RNA. The polymerase chain reaction may also be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the instant nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, the skilled artisan can follow the RACE protocol (Frohman et al. (1988) *Proc. Natl. Acad. Sci. USA 85*:8998-9002) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant sequences. Using commercially available 3' RACE or 5' RACE systems (BRL), specific 3' or 5' cDNA fragments can be isolated (Ohara et al. (1989) *Proc. Natl. Acad. Sci. USA 86*:5673-5677; Loh et al. (1989) *Science 243*:217-220). Products generated by the 3' and 5' RACE procedures can be combined to generate full-length cDNAs (Frohman and Martin (1989) *Techniques 1*:165). Consequently, a polynucleotide comprising a nucleotide sequence of at least 30 (preferably at least 40, most preferably at least 60) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 and the complement of such nucleotide sequences may be used in such methods to obtain a nucleic acid fragment encoding a substantial portion of an amino acid sequence of a polypeptide. The present invention relates to a method of obtaining a nucleic acid fragment encoding a substantial portion of a polypeptide of a gene (such as diacylglycerol acyltransferases) preferably a substantial portion of a plant polypeptide of a gene, comprising the steps of: synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least 30 (preferably at least 40, most preferably at least 60) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences; and amplifying a nucleic acid fragment (preferably a cDNA inserted in a cloning vector) using the oligonucleotide primer. The amplified nucleic acid fragment preferably will encode a portion of a polypeptide.

IN THE CLAIMS

Please cancel claims 1-25.

Please add the following new claims:

--26. An isolated polynucleotide that encodes a diacylglycerol acyltransferase having a sequence identity of at least 85% based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 14, 16, 18, 20 and 22.

27. A polynucleotide sequence of Claim 26, wherein the sequence identity is at least 90%.

28. A polynucleotide sequence of Claim 26, wherein the sequence identity is at least 95%.

29. The polynucleotide of Claim 26 wherein the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 22.

30. The polynucleotide of Claim 26, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 21.

31. An isolated complement of the polynucleotide of Claim 26, wherein (a) the complement and the polynucleotide consist of the same number of nucleotides, and (b) the nucleotide sequences of the complement and the polynucleotide have 100% complementarity.

A4 cont'd

32. An isolated nucleic acid molecule that (1) comprises at least 30 nucleotides and (2) remain hybridized with the isolated polynucleotide of Claim 26 under a wash condition of 0.1X SSC, 0.1% SDS, and 65°C.

33. A cell comprising the polynucleotide of Claim 26.

34. The cell of Claim 33, wherein the cell is selected from the group consisting of a yeast cell, a bacterial cell and a plant cell.

35. A transgenic plant comprising the polynucleotide of Claim 26.

36. A method for transforming a cell comprising introducing into a cell the polynucleotide of Claim 26.

37. A method for producing a transgenic plant comprising (a) transforming a plant cell with the polynucleotide of Claim 26, and (b) regenerating a plant from the transformed plant cell.

38. A method for producing a polynucleotide fragment comprising (a) selecting a nucleotide sequence comprised by the polynucleotide of Claim 26, and (b) synthesizing a polynucleotide fragment containing the nucleotide sequence.

39. The method of Claim 38, wherein the fragment is produced *in vivo*.

40. An isolated diacylglycerol acyltransferase polypeptide having a sequence identity of at least 85% based on the Clustal method compared to an amino acid sequence selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 22.

41. The polypeptide of Claim 40, wherein the sequence identity is at least 90%.

42. The polypeptide of Claim 40, wherein the sequence identity is at least 95%.

43. The polypeptide of Claim 40 wherein the polypeptide has a sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 22.

44. A chimeric gene comprising the polynucleotide of Claim 26 operably linked to at least one suitable regulatory sequence.

45. A method for altering the level of diacylglycerol acyltransferase expression in a host cell, the method comprising:

(a) Transforming a host cell with the chimeric gene of claim 44; and
(b) Growing the transformed cell in step (a) under conditions suitable for the expression of the chimeric gene.--

A4 cont'd

Remarks

Applicants respectfully submit that the amendments to the Specification only correct obvious typographical and clerical errors. Furthermore, applicants submit that amended and newly added claims more clearly and distinctly recite that which applicants consider to be their invention, and are adequately supported by the original disclosure. No new matter is believed to be at issue. Entry of the amendments and early favorable consideration of the claims are hereby respectfully requested.

Respectfully submitted,

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